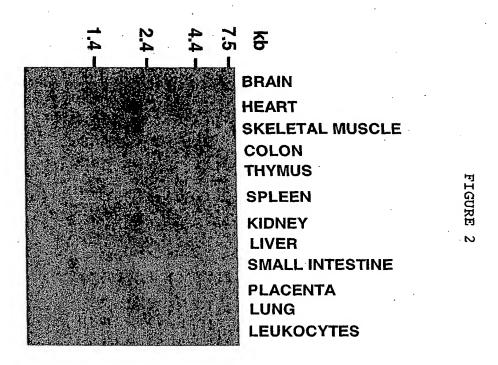
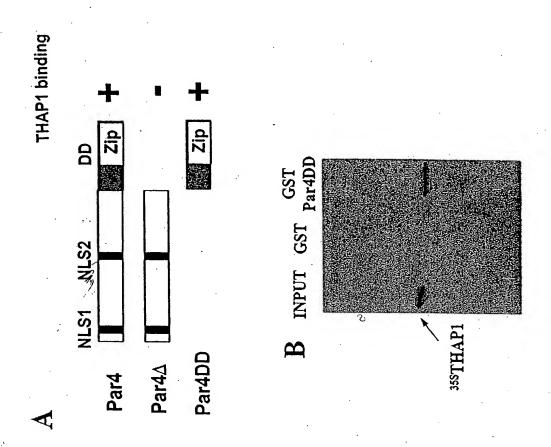
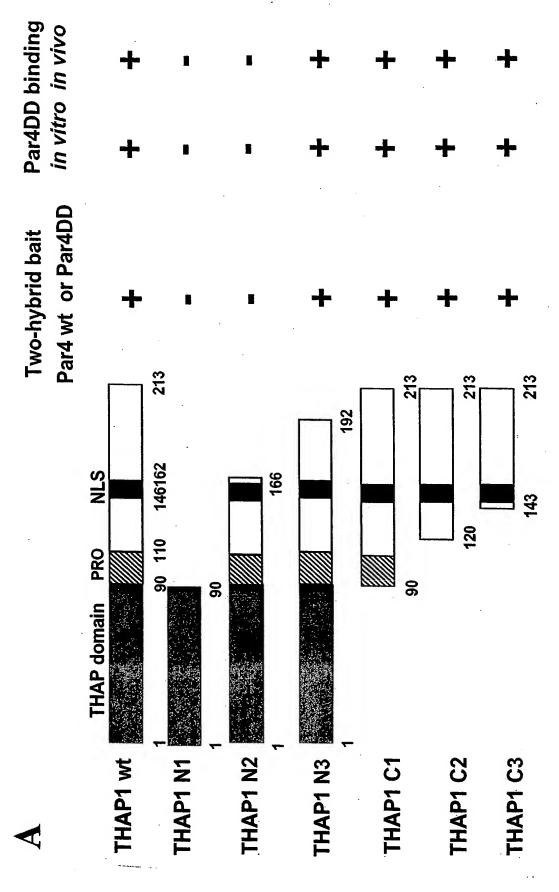


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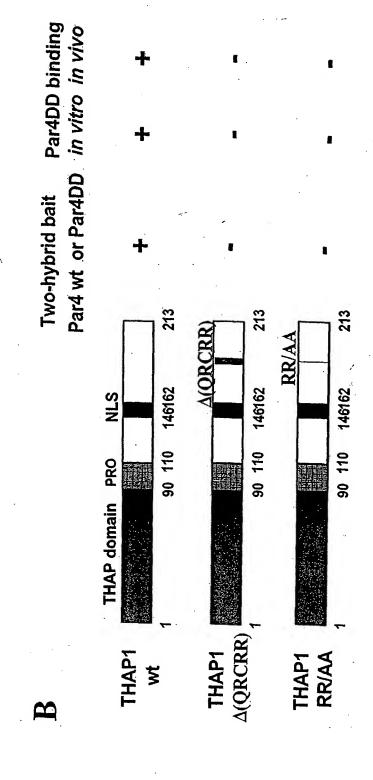


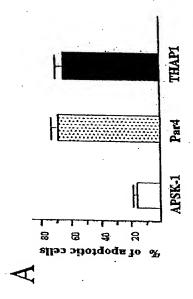
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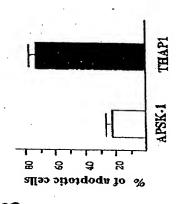
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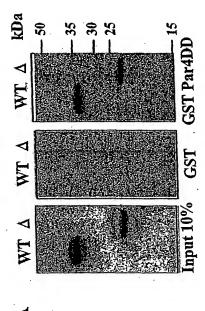
-VLEDVAAAEOGLREL--QRGRRQCRERVCALRAAAEQREARCRDG -QLEQQVEKLRKKLKTAQQRCRRQERQLEKLKEVVHFQREKDDASE -Q**le**Qoveklrkklktaq**qr**c**rrq**e**r**qleklkevvhf**q**k**e**kddvse mZIP mTHAP-1 hTHAP-1

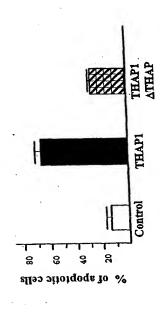
Consensus Par4 binding site: LE (X₁₂₋₁₄) QRXRRQXR (X₁₁) QXE

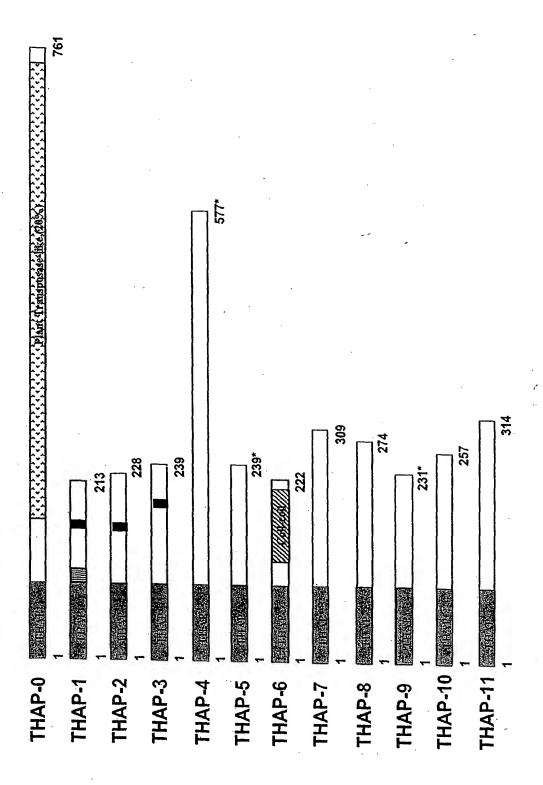












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FIG. 9C

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FIG. 9C

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Figure 10

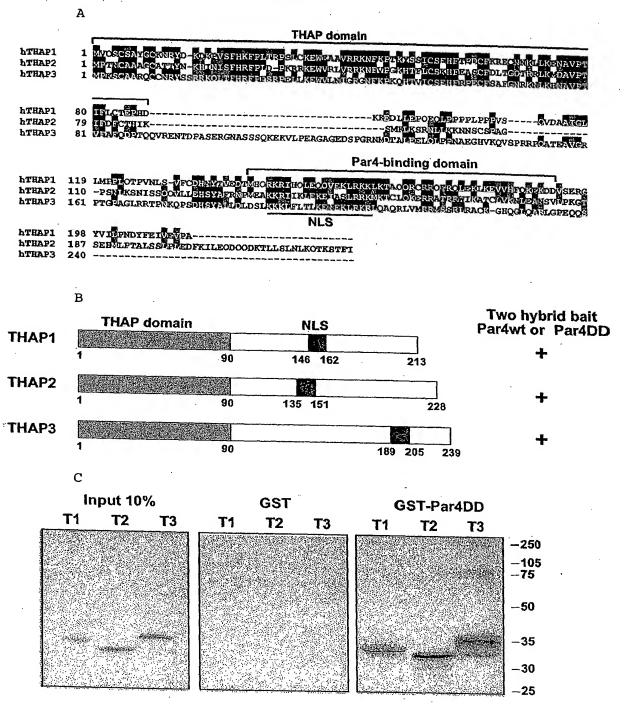
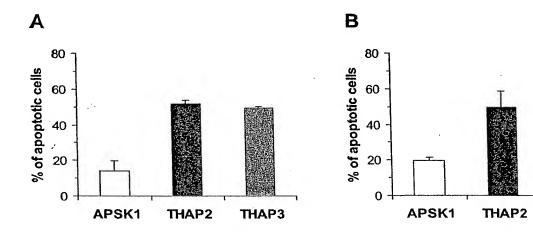
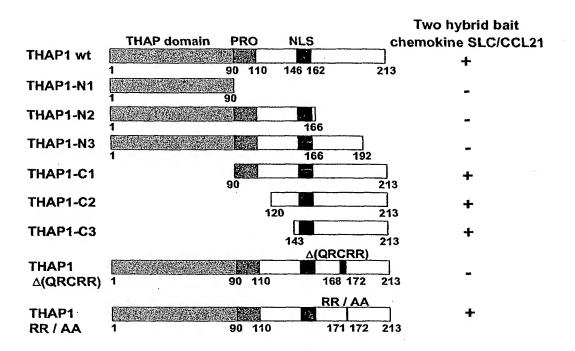


Figure 11



THAP3

Figure 12



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Figure 13

	CCR7-binding domain	SLC-specific basic extension	Two hybrid bait THAP1	In vitro binding to GST-THAP1
SLC/CCL21 wt	24	102 134	+	+
SLC/CCL21	24	102	+	+

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FIGURE 14

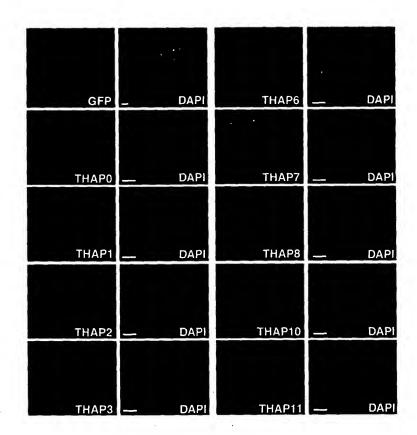
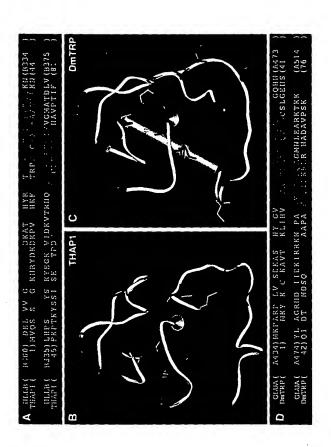
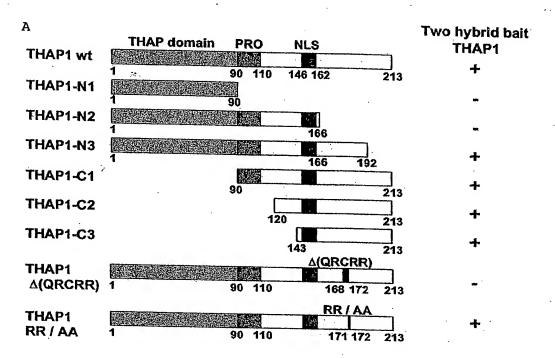


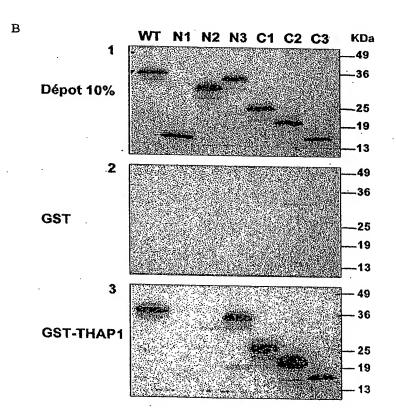
FIGURE 15



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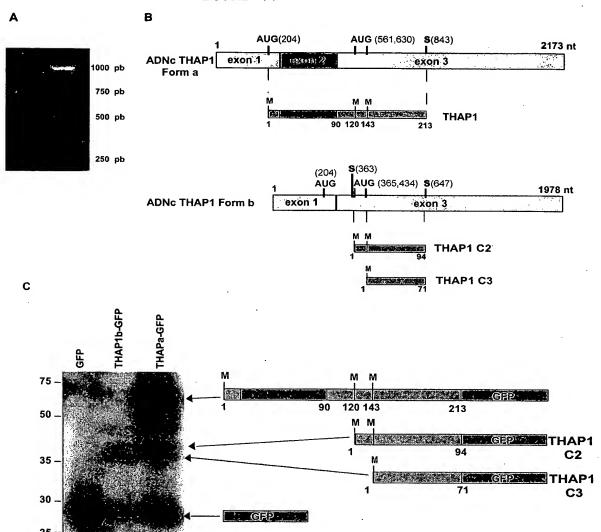
FIGURE 16





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FIGURE 17



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Figure 18

ACTGT GGGCAT	ACTAC TGGCAA	ACTAC TGGCAA	GTTCG TTGCAA	GTAC TGGCAA	CIGT GGGCAA	CACTAC TGGCAA	AGTAC TGGCAA
GGGCAA	GGGCAT	GGGCAA	GGGCCA	GGGCAT	GGGCAA	GGGCAA	GGGCAA

1) DR-5 Consensus Motif

666CAAnnnnT66CAA

(DR-4, DR-6)

	GGGCAG	GTAGTAAGTGT	CTGCCA
	GGGCAG	GTAGTTAGTGT	TIGCCA
]	GGGCAA	GTACCTACTAA	TIGCCA
	GGGCAA	GTAGTTAGTGT	TIGCCA
	GGGCGA	GTAGTTAGGTGT	TIGCCA
	GGGCAA	GTAGATACTGT	CIGCCA
L	GGGCAA	GTACTAAGTGT	TIGCCA
	GGGCAA	GTACATAGTGT	CIGCCA
	GGGCAA	GTACTAAGTGT	TTGCCA

2) ER-11 Consensus Motif	TTGCCAnnnnnnnnnnGGGCAA (ER-12)
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Figure 19

